



SEQUENCE LISTING

#4

<110> DeVico, Anthony L.

Fouts, Timothy R.

Tuskan, Robert G.

<120> VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE

<130> 4115-144 CIP

<140> US 09/934,060

<141> 2001-08-21

<150> US 09/684,026

<151> 2000-10-06

<150> US 60/158,321

<151> 1999-10-08

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 2159

<212> DNA

<213> Artificial Sequence

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<223> Synthesized construct

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cacgaggaca tcatcagcct gtgggaccag agcctgaagc cctgcgtgaa gctgaccccc	360
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agtggcacct ggacatgcac tgtcttgcaag aaccagaaga aggtggagtt caaaatagac	2100
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<210> 2

<211> 720

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<220>

<221> MISC_FEATURE

<222> (716)..(716)

<223> Xaa can be any amino acid

<220>

<221> MISC_FEATURE

<222> (719)..(719)

<223> Xaa can be any amino acid

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 Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
 35 40 45
 Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
 50 55 60
 Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
 65 70 75 80
 Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
 85 90 95
 Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
 100 105 110
 Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
 115 120 125
 Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
 130 135 140
 Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
 145 150 155 160
 Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
 165 170 175
 Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
 180 185 190
 Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
 195 200 205
 Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
 210 215 220
 Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys

225		230		235		240
Thr Asn Val Ser	Thr Val Gln Cys	Thr His Gly Ile Arg	Pro Val Val			
	245	250	255			
Ser Thr Gln Leu	Leu Leu Asn Gly	Ser Leu Ala Glu	Glu Glu Val Val			
	260	265	270			
Ile Arg Ser Ala	Asn Phe Ala Asp	Asn Ala Lys Val	Ile Ile Val Gln			
	275	280	285			
Leu Asn Glu Ser	Val Glu Ile Asn	Cys Thr Arg Pro	Asn Asn Asn Thr			
	290	295	300			
Arg Lys Ser Ile	His Ile Gly Pro	Gly Arg Ala Phe	Tyr Thr Thr Gly			
305	310	315	320			
Glu Ile Ile Gly	Asp Ile Arg Gln	Ala His Cys Asn	Leu Ser Arg Ala			
	325	330	335			
Lys Trp Asn Asp	Thr Leu Asn Lys	Ile Val Ile Lys	Leu Arg Glu Gln			
	340	345	350			
Phe Gly Asn Lys	Thr Ile Val Phe	Lys His Ser Ser	Gly Gly Asp Pro			
	355	360	365			
Glu Ile Val Thr	His Ser Phe Asn	Cys Gly Gly Glu	Phe Phe Tyr Cys			
	370	375	380			
Asn Ser Thr Gln	Leu Phe Asn Ser	Thr Trp Asn Val	Thr Glu Glu Ser			
385	390	395	400			
Asn Asn Thr Val	Glu Asn Asn Thr	Ile Thr Leu Pro	Cys Arg Ile Lys			
	405	410	415			
Gln Ile Ile Asn	Met Trp Gln Glu	Val Gly Arg Ala	Met Tyr Ala Pro			
	420	425	430			
Pro Ile Arg Gly	Gln Ile Arg Cys	Ser Ser Asn Ile	Thr Gly Leu Leu			
	435	440	445			
Leu Thr Arg Asp	Gly Gly Pro Glu	Asp Asn Lys Thr	Glu Val Phe Arg			
	450	455	460			

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
 465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
 485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Arg Gly Ser Ser Gly Gly Gly
 500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys
 515 520 525

Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr
 530 535 540

Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln
 545 550 555 560

Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser
 565 570 575

Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly
 580 585 590

Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr
 595 600 605

Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val
 610 615 620

Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser
 625 630 635 640

Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln
 645 650 655

Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser
 660 665 670

Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val
 675 680 685

Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu
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<213> Artificial Sequence

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<223> Synthesized construct

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tggaaggagg ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag	180
gtgcacaacg tgtggggccac ccacgcctgc gtgcccaccg accccaaccc ccaggaggtg	240
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<221> MISC_FEATURE

<222> (716)..(716)

<223> Xaa can be any amino acid

<220>

<221> MISC_FEATURE

<222> (719)..(719)

<223> Xaa can be any amino acid

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Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
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Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn

145		150		155		160
Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe	165		170		175	
Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr	180		185		190	
Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys	195		200		205	
Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe	210		215		220	
Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys	225		230		235	240
Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val	245		250		255	
Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val	260		265		270	
Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln	275		280		285	
Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr	290		295		300	
Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly	305		310		315	320
Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala	325		330		335	
Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln	340		345		350	
Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro	355		360		365	
Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys	370		375		380	

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
 385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys
 405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
 420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
 435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
 450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
 465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
 485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr Gly Ser Ser Gly Gly Gly
 500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys
 515 520 525

Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr
 530 535 540

Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln
 545 550 555 560

Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser
 565 570 575

Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly
 580 585 590

Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr
 595 600 605

Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val
610 615 620

Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser
625 630 635 640

Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln
645 650 655

Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser
660 665 670

Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val
675 680 685

Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu
690 695 700

Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr
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accctgaaca agatcgtgat caagctgcgc gagcagttcg gcaacaagac catcgtgttc	1080
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<211> 556

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<222> (556)..(556)

<223> Xaa can be any amino acid

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Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
 180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
 195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
 210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys
 225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
 245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
 260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln
 275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
 290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
 305 310 315 320

Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala
 325 330 335

Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln
 340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro
 355 360 365

Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
 370 375 380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
 385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys

405

410

415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
 420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
 435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
 450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
 465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
 485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr Gly Ser Ser Gly Gly Gly
 500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Cys
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Asn Leu Ala Arg Cys Gln Leu Arg Cys Lys Ser Leu Gly Leu Leu Gly
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Lys Cys Ala Gly Ser Phe Cys Ala Cys Gly Pro Xaa
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<221> primer_bind

<222> (1)..(39)

<223>

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<211> 66

<212> DNA

<213> Artificial Sequence

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gcgctt

66

<210> 9

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<220>

<221> primer_bind

<222> (1)..(69)

<223>

<400> 9

gggtccggag gaggtgggtc ggggtggcggc gcggccgcta agaaagtggg gctgggcaaa

60

aaaggggat

69

<210> 10

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<220>

<221> primer_bind

<222> (1)..(76)

<223>

<400> 10

ggggttttaa cttattacag atcctcttct gagatgagtt ttgttcagct agcaccacga

60

tgtctatttt gaactc

76

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<220>

<221> misc_feature

<222> (1)..(21)

<223> Spacer

<400> 11
gssggggsgs gggsggggaa a

21

<210> 12

<211> 1769

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 12
atgcccatgg ggtctctgca accgctggcc acctgtacc tgctggggat gctggtcgct 60
tcctgcctcg gaaagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 120
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 180
acccccctgt gcgtgaccct gggcgcgggc gagatgaaga actgcagctt caacatcggc 240
gcgggcccgc tgatcagctg caacaccagc gtgatcacc aggctgccc caaggtgagc 300
ttcgagccca tccccatcca ctactgcgc cccgccggct tcgccatcct gaagtgaag 360
gacaagaagt tcaacggcaa gggcccctgc accaacgtga gcaccgtgca gtgcaccac 420
ggcatccgcc ccgtggtgag caccagctg ctgctgaacg gcagcctggc cgaggaggag 480
gtggtgatcc gcagcgccaa cttcgccgac aacgccaaagg tgatcatcgt gcagctgaac 540
gagagcgtgg agatcaactg caccgcggcc aacaacaaca cccgcaagtc catccacatc 600
ggccccggcc gcgccttcta caccaccggc gagatcatcg gcgacatccg ccaggccac 660
tgcaacctga gccgcgcca gtggaacgac accctgaaca agatcgtgat caagctgcgc 720
gagcagttcg gcaacaagac catcgtgttc aagcacagca gcggcggcga ccccgagatc 780
gtgaccacac gcttcaattg cggcggcgag ttcttctact gcaacagcac ccagctgttc 840
aacagcacct ggaacgtgac cgaggagagc aacaacaccg tggagaacaa caccatcacc 900
ctgccctgcc gcatcaagca gatcatcaac atgtggcagg aggtgggccc cgccatgtac 960
gccccccca tccgcggcca gatccgtgc agttchaaca tcaccggcct gctgctgacc 1020
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cgcgacaact ggcgcagcga gctgtacaag tacaaggtgg tgaagatcgg atcctctggg 1140

ggcgggtggct cgggctccgg aggaggtggg tcgggtggcg gcgcggccgc taagaaagtg	1200
gtgctgggca aaaaagggga tacagtggaa ctgacctgta cagcttccca gaagaagagc	1260
atacaattcc actggaaaaa ctccaaccag ataaagattc tgggaaatca gggctccttc	1320
ttaactaaag gtccatccaa gctgaatgat cgcgctgact caagaagaag cctttgggac	1380
caaggaaaact tccccctgat catcaagaat cttaagatag aagactcaga tacttacatc	1440
tgtgaagtgg aggaccagaa ggaggaggtg caattgctag tgttcggatt gactgccaac	1500
tctgacaccc acctgcttca ggggcagagc ctgaccctga ccttggagag cccccctggt	1560
agtagcccct cagtgcaatg taggagtcca aggggtaaaa acatacaggg ggggaagacc	1620
ctctccgtgt ctgagctgga gctccaggat agtggcacct ggacatgcac tgtcttgcat	1680
aaccagaaga aggtggagtt caaaatagac atcgtggtgc tagctgaaca aaaactcatc	1740
tcagaagagg atctgtaata tgtttaaac	1769

<210> 13

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<220>

<221> MISC_FEATURE

<222> (586)..(586)

<223> Xaa can be any amino acid

<220>

<221> MISC_FEATURE

<222> (589)..(589)

<223> Xaa can be any amino acid

<400> 13

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Lys Asn Val Thr Glu Asn Phe Asn
20 25 30

Met Trp Lys Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser
35 40 45

Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys
50 55 60

Val Thr Leu Gly Ala Gly Glu Met Lys Asn Cys Ser Phe Asn Ile Gly
65 70 75 80

Ala Gly Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys
85 90 95

Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
100 105 110

Gly Phe Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly
115 120 125

Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro
130 135 140

Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu
145 150 155 160

Val Val Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile
165 170 175

Val Gln Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn
180 185 190

Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr
195 200 205

Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser
210 215 220

Arg Ala Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg
225 230 235 240

Glu Gln Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly
245 250 255

Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe
260 265 270

Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu
275 280 285

Glu Ser Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg
290 295 300

Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr
305 310 315 320

Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly
325 330 335

Leu Leu Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val
340 345 350

Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu
355 360 365

Tyr Lys Tyr Lys Val Val Lys Ile Gly Ser Ser Gly Gly Gly Gly Ser
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys Lys Val
385 390 395 400

Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser
405 410 415

Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys
420 425 430

Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu
435 440 445

Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe
450 455 460

Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile
465 470 475 480

Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly
485 490 495

Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr
500 505 510

Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg
515 520 525

Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser
530 535 540

Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln
545 550 555 560

Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Glu
565 570 575

Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr
580 585 590

<210> 14

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> Xaa can be any amino acid

<220>

<221> MISC_FEATURE

<222> (14)..(14)

<223> Xaa can be any amino acid

<400> 14

Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Xaa	Tyr	Val	Xaa	Thr
1				5					10				15	

<210> 15

<211> 111

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 15	
gggggtacca tgcccatggg gtctctgcaa ccgctggcca ccttgtagct gctggggatg	60
ctggtcgctt cctgcctcgg aaagaacgtg accgagaact tcaacatgtg g	111

<210> 16

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 16	
gggggatccg atcttcacca ccttgatctt gtacagctc	39

<210> 17

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 17
ctgtgcgtga ccctgggagc ggccgagatg aagaactgca gcttcaacat cggcgcgggc 60
cgctgatca gctgc 75

<210> 18

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 18
gcagctgac aggcggcccg cgccgatgtt gaagctgcag ttcttcatct cgcccgcgcc 60
cagggtcacg cacag 75

<210> 19

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 19
tgcaacctgg cccgctgcca gctgcgctgc aagagcctgg gcctgctggg caagtgcgcc 60

ggcagcttct gcgcctgcgg cccctaa

87

<210> 20

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 20

Cys	Asn	Leu	Ala	Arg	Cys	Gln	Leu	Arg	Cys	Lys	Ser	Leu	Gly	Leu	Leu
1				5				10					15		

Gly	Lys	Cys	Ala	Gly	Ser	Phe	Cys	Ala	Cys	Gly	Pro
			20				25				

<210> 21

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 21

gcggccgctt gcaacctggc ccgctgccag ctgcgctgca agagcctggg cctgctgggc 60

aagtgcgccg gcagcttctg cgcctgcggc ccctaagaat tc 102

<210> 22

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 22
gaattcttag gggccgcagg cgcagaagct gccggcgcac ttgccagca ggcccaggct 60
cttgacgcgc agctggcagc gggccagggt gcaagcggcc gc 102

<210> 23

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 23
atgcccatgg ggtctctgca accgctggcc acctgtacc tgctggggat gctggtcgct 60
tcctgcctcg gaaacgccga ggagaagctg tgggtgaccg tgtactacgg cgtgcccgtg 120
tggaaggagg ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag 180
gtgcacaacg tgtgggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagggtg 240
gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggg ggagcagatg 300
cacgaggaca tcatcagcct gtgggaccag agcctgaagc cctgcggtgaa gctgaccccc 360
ctgtgcgtga ccctgaactg caccgacctg cgcaacgcc acaacggcaa cgacaccaac 420
accactagta gcagccgcgg catggtgggc ggccggcgaga tgaagaactg cagcttcaac 480
atcaccacca acatccgcgg caaggtgcag aaggagtacg ccctgttcta caagctggac 540
atcgccccca tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc 600
gtgatcacc ccagcctgccc caaggtgagc ttcgagccca tccccatcca ctactgcgcc 660
cccgccgggt tcgccatcct gaagtgaag gacaagaagt tcaacggcaa gggcccctgc 720
accaacgtga gcaccgtgca gtgcaccac ggcacccgcc ccgtggtgag caccagctg 780
ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgcaa cttcgccgac 840
aacgccaagg tgatcatcgt gcagctgaac gagagcgtgg agatcaactg caccgcccc 900
aacaacaaca cccgcaagtc catccacatc ggccccggcc gcgccttcta caccaccggc 960

gagatcatcg gcgacatccg ccaggccac tgcaacctga gccgcgcaa gtggaacgac 1020
accctgaaca agatcgtgat caagctgcmc gagcagttcg gcaacaagac catcgtgttc 1080
aagcacagca gcggcggcga ccccgagatc gtgaccacaca gcttcaattg cggcggcgag 1140
ttcttctact gcaacagcac ccagctgttc aacagcacct ggaacgtgac cgaggagagc 1200
aacaacaccg tggagaacaa caccatcacc ctgccctgcc gcatcaagca gatcatcaac 1260
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gaggtgttcc gccccggcgg cggcgacatg cgcgacaact ggcgacgcga gctgtacaag 1440
tacaaggctg tgaagatcga gccctgggc gtggcccca ccaaggcaa gcgccgcgtg 1500
gtgcagcgcg agaagcgt 1518

<210> 24

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 24

Met	Pro	Met	Gly	Ser	Leu	Gln	Pro	Leu	Ala	Thr	Leu	Tyr	Leu	Leu	Gly
1				5					10					15	

Met	Leu	Val	Ala	Ser	Cys	Leu	Gly	Asn	Ala	Glu	Glu	Lys	Leu	Trp	Val
			20					25					30		

Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	Lys	Glu	Ala	Thr	Thr	Thr	Leu
		35					40					45			

Phe	Cys	Ala	Ser	Asp	Arg	Lys	Ala	Tyr	Asp	Thr	Glu	Val	His	Asn	Val
	50					55					60				

Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Asp	Pro	Asn	Pro	Gln	Glu	Val
65					70					75				80	

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys
225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln
275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly

305 310 315 320
 Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala
 325 330 335
 Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln
 340 345 350
 Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro
 355 360 365
 Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
 370 375 380
 Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
 385 390 395 400
 Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys
 405 410 415
 Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
 420 425 430
 Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
 435 440 445
 Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
 450 455 460
 Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
 465 470 475 480
 Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
 485 490 495
 Lys Arg Arg Val Val Gln Arg Glu Lys Arg
 500 505

<210> 25

<211> 534

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 25
aagaaagtgg tgctgggcaa aaaaggggat acagtggaac tgacctgtac agcttcccag 60
aagaagagca tacaattcca ctggaaaaac tccaaccaga taaagattct gggaaatcag 120
ggctccttct taactaaagg tccatccaag ctgaatgata gcgctgactc aagaagaagc 180
ctttgggacc aaggaaactt cccctgatac atcaagaatc ttaagataga agactcagat 240
acttacatct gtgaagtgga ggaccagaag gaggaggtgc aattgctagt gttcggattg 300
actgccaact ctgacacca cctgcttcag gggcagagcc tgacctgac cttggagagc 360
cccctggta gtagccctc agtgcaatgt aggagtcaa ggggtaaaaa catacagggg 420
gggaagaccc tctccgtgtc tcagctggag ctccaggata gtggcacctg gacatgcact 480
gtcttgacga accagaagaa ggtggagttc aaaatagaca tcgtggtgct agct 534

<210> 26

<211> 178

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 26

Lys	Lys	Val	Val	Leu	Gly	Lys	Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys
1				5					10					15	

Thr	Ala	Ser	Gln	Lys	Lys	Ser	Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn
			20					25					30		

Gln	Ile	Lys	Ile	Leu	Gly	Asn	Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro
		35					40					45			

Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln

50

55

60

Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp
65 70 75 80

Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu
85 90 95

Val Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln
100 105 110

Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val
115 120 125

Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu
130 135 140

Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr
145 150 155 160

Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val
165 170 175

Leu Ala

<210> 27

<211> 1128

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 27
atgcccatgg ggtctctgca accgctggcc accttgtagc tgctggggat gctggctgct 60
tcttgccctcg gaaagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 120
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 180
acccccctgt gcgtgaccct gggcgcgggc gagatgaaga actgcagctt caacatcggc 240

gcggggccgcc tgatcagctg caacaccagc gtgatcacc aggctgccc caaggtgagc 300
 ttcgagccca tccccatcca ctactgcgcc cccgccggct tcgccatcct gaagtgcaag 360
 gacaagaagt tcaacggcaa gggcccctgc accaacgtga gcaccgtgca gtgcacccac 420
 ggcatccgcc ccgtggtgag caccagctg ctgctgaacg gcagcctggc cgaggaggag 480
 gtggtgatcc gcagcgccaa cttcgccgac aacgccaagg tgatcatcgt gcagctgaac 540
 gagagcgtgg agatcaactg caccgcccc aacaacaaca cccgcaagtc catccacatc 600
 ggccccggcc gcgccttcta caccaccggc gagatcatcg gcgacatccg ccaggccccac 660
 tgcaacctga gccgcgcaa gtggaacgac accctgaaca agatcgtgat caagctgcgc 720
 gagcagttcg gcaacaagac catcgtgttc aagcacagca gcggcgggcg ccccgagatc 780
 gtgaccaca gcttcaattg cggcgggcag ttcttctact gcaacagcac ccagctgttc 840
 aacagcacct ggaacgtgac cgaggagagc aacaacaccg tggagaaaa caccatcacc 900
 ctgccctgcc gcatcaagca gatcatcaac atgtggcagg aggtgggccc cgccatgtac 960
 gcccccccca tccgcggcca gatccgctgc agttchaaca tcaccggcct gctgctgacc 1020
 cgcgacggcg gccccgagga caacaagacc gaggtgttcc gccccggcgg cggcgacatg 1080
 cgcgacaact ggcgcagcga gctgtacaag tacaaggtgg tgaagatc 1128

<210> 28

<211> 376

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 28

Met	Pro	Met	Gly	Ser	Leu	Gln	Pro	Leu	Ala	Thr	Leu	Tyr	Leu	Leu	Gly
1				5					10					15	

Met	Leu	Val	Ala	Ser	Cys	Leu	Gly	Lys	Asn	Val	Thr	Glu	Asn	Phe	Asn
			20					25					30		

Met Trp Lys Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser

35

40

45

Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys
50 55 60

Val Thr Leu Gly Ala Gly Glu Met Lys Asn Cys Ser Phe Asn Ile Gly
65 70 75 80

Ala Gly Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys
85 90 95

Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
100 105 110

Gly Phe Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly
115 120 125

Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro
130 135 140

Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu
145 150 155 160

Val Val Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile
165 170 175

Val Gln Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn
180 185 190

Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr
195 200 205

Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser
210 215 220

Arg Ala Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg
225 230 235 240

Glu Gln Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly
245 250 255

Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe
260 265 270

Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu
 275 280 285

Glu Ser Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg
 290 295 300

Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr
 305 310 315 320

Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly
 325 330 335

Leu Leu Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val
 340 345 350

Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu
 355 360 365

Tyr Lys Tyr Lys Val Val Lys Ile
 370 375

<210> 29

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 29
 atgcccatgg ggtctctgca accgctggcc accttgtagc tgctggggat gctgggtcgct 60
 tctgcctcg gaaacgccga ggagaagctg tgggtgaccg tgtactacgg cgtgcccgtg 120
 tggaaggagg ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag 180
 gtgcacaacg tgtggggccac ccacgcctgc gtgcccaccg accccaaccc ccaggaggtg 240
 gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggt ggagcagatg 300
 cacgaggaca tcatcagcct gtgggaccag agcctgaagc cctgcgtgaa gctgaccccc 360

ctgtgctga ccctgaactg caccgacctg cgcaacgcc ccaacggcaa cgacaccaac	420
accactagta gcagccgcgg catggtgggc ggcggcgaga tgaagaactg cagcttcaac	480
atcaccacca acatccgcgg caaggtgcag aaggagtacg ccctgttcta caagctggac	540
atcgccccca tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc	600
gtgatcacc aggctgccc caaggtgagc ttcgagccca tccccatcca ctactgcgcc	660
cccgcgggt tcgccatcct gaagtgcag gacaagaagt tcaacggcaa gggcccctgc	720
accaacgtga gcaccgtgca gtgcaccac ggcatccgcc ccgtggtgag caccagctg	780
ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgcaa cttcgccgac	840
aacgccaagg tgatcatcgt gcagctgaac gagagcgtgg agatcaactg caccgcccc	900
aacaacaaca cccgcaagtc catccacatc ggccccggcc ggccttcta caccaccggc	960
gagatcatcg gcgacatccg ccaggccac tgcaacctga gccgcgcaa gtggaacgac	1020
accctgaaca agatcgtgat caagctgagc gagcagttcg gcaacaagac catcgtgttc	1080
aagcacagca gcggcggcga ccccgagatc gtgaccaca gcttcaattg cggcggcgag	1140
ttcttctact gcaacagcac ccagctgttc aacagcacct ggaacgtgac cgaggagagc	1200
aacaacaccg tggagaacaa caccatcacc ctgccctgcc gcatcaagca gatcatcaac	1260
atgtggcagg aggtgggccc cgccatgtac gccccccca tccgcggcca gatccgctgc	1320
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gaggtgttcc gccccggcgg cggcgacatg cgcgacaact ggcgcagcga gctgtacaag	1440
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<210> 30

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 30

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 20 25 30
 Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
 35 40 45
 Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
 50 55 60
 Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
 65 70 75 80
 Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
 85 90 95
 Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
 100 105 110
 Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
 115 120 125
 Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
 130 135 140
 Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
 145 150 155 160
 Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
 165 170 175
 Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
 180 185 190
 Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
 195 200 205
 Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
 210 215 220
 Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys

225		230		235		240									
Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val
				245					250					255	
Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val
			260					265					270		
Ile	Arg	Ser	Ala	Asn	Phe	Ala	Asp	Asn	Ala	Lys	Val	Ile	Ile	Val	Gln
		275					280					285			
Leu	Asn	Glu	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr
	290					295					300				
Arg	Lys	Ser	Ile	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly
305					310					315					320
Glu	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala
				325					330					335	
Lys	Trp	Asn	Asp	Thr	Leu	Asn	Lys	Ile	Val	Ile	Lys	Leu	Arg	Glu	Gln
			340					345					350		
Phe	Gly	Asn	Lys	Thr	Ile	Val	Phe	Lys	His	Ser	Ser	Gly	Gly	Asp	Pro
		355					360					365			
Glu	Ile	Val	Thr	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys
	370						375				380				
Asn	Ser	Thr	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Val	Thr	Glu	Glu	Ser
385					390					395					400
Asn	Asn	Thr	Val	Glu	Asn	Asn	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys
				405					410					415	
Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Arg	Ala	Met	Tyr	Ala	Pro
			420					425					430		
Pro	Ile	Arg	Gly	Gln	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu
		435					440					445			
Leu	Thr	Arg	Asp	Gly	Gly	Pro	Glu	Asp	Asn	Lys	Thr	Glu	Val	Phe	Arg
	450					455					460				

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
 465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
 485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr
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<210> 31

<211> 776

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 31
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 tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaaccaag 180
 gacaccctca tgatctcccg gaccctgag gtcacatgcg tggtggtgga cgtgagccac 240
 gaagaccctg aggtcaagtt caactggtac gtggacggcg tggagggtgca taatgccaag 300
 acaaagccgc gggaggagca gtacaacagc acgtaccggg tggtcagcgt cctcacgctc 360
 ctgcaccagg actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc 420
 ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacagggtg 480
 tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 540
 gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 600
 aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 660
 aagctcaccg tggacaagag cagggtggcag caggggaacg tcttctcatg ctccgtgatg 720
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<210> 32

<211> 259

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<220>

<221> MISC_FEATURE

<222> (259)..(259)

<223> Xaa can be any amino acid

<400> 32

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
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Met Leu Val Ala Ser Val Leu Ala Asp Pro Glu Glu Pro Lys Ser Cys
20 25 30

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
35 40 45

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
50 55 60

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
65 70 75 80

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
85 90 95

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
100 105 110

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
115 120 125

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 130 135 140

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 145 150 155 160

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 165 170 175

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 180 185 190

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 195 200 205

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 210 215 220

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 225 230 235 240

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 245 250 255

Pro Gly Xaa

<210> 33

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 33

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gct 63